



# STIC Search Report

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**TO: Jeanine Goldberg**  
**Location: mail 12E12; room 12D11**  
**Art Unit: 1634**  
**Friday, May 30, 2003**

**Case Serial Number: 807506**

**From: Barb O'Bryen**  
**Location: Biotech-Chem Library**  
**CM1-6A05**  
**Phone: 308-4291** *BOB*

**barbara.obryen@uspto.gov**

### Search Notes

#### O'Bryen, Barbara

**From:** Goldberg, Jeanine  
**Sent:** Wednesday, May 21, 2003 2:07 PM  
**To:** O'Bryen, Barbara  
**Subject:** 09/807,506- biallelic schizophrenia

1. please search SEQ ID NO: 35.

THANK YOU  
Jeanine

Jeanine Enewold Goldberg  
1634  
CM1--12D11  
Mailbox-- 12E12  
306-5817

L4 ANSWER 1 OF 41 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
1

ACCESSION NUMBER: 2003:248639 BIOSIS  
DOCUMENT NUMBER: PREV200300248639  
TITLE: Schizophrenia associated gene, proteins and  
**biallelic** markers.  
AUTHOR(S): Cohen, Daniel (1); Blumenfeld, Marta; Chumakov, Ilya;  
Bougueleret, Lydie; Essioux, Laurent  
CORPORATE SOURCE: (1) Neuilly-sur-Seine, France France  
ASSIGNEE: Genset S.A., France  
PATENT INFORMATION: US 6555316 April 29, 2003  
SOURCE: Official Gazette of the United States Patent and Trademark  
Office Patents, (Apr. 29 2003) Vol. 1269, No. 5, pp. No  
Pagination. <http://www.uspto.gov/web/menu/patdata.html>.  
e-file.  
ISSN: 0098-1133.

DOCUMENT TYPE: Patent  
LANGUAGE: English

AB The invention concerns the human g35030 gene, polynucleotides,  
polypeptides **biallelic** markers, and human chromosome  
**13q31-q33 biallelic** markers. The invention also concerns  
the association established between schizophrenia and bipolar disorder and  
the **biallelic** markers and the g35030 gene and nucleotide  
sequences. The invention provides means to identify compounds useful in  
the treatment of schizophrenia, bipolar disorder and related diseases,  
means to determine the predisposition of individuals to said disease as  
well as means for the disease diagnosis and prognosis.

L4 ANSWER 2 OF 41 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 2003185197 MEDLINE  
DOCUMENT NUMBER: 22589958 PubMed ID: 12647258  
TITLE: Polymorphisms at the G72/G30 gene locus, on **13q33**  
, are associated with bipolar disorder in two independent  
pedigree series.  
AUTHOR: Hattori Eiji; Liu Chunyu; Badner Judith A; Bonner Tom I;  
Christian Susan L; Maheshwari Manjula; Detera-Wadleigh  
Sevilla D; Gibbs Richard A; Gershon Elliot S  
CORPORATE SOURCE: Department of Psychiatry, The University of Chicago, IL  
60637, USA.. ehattori@yoda.bsd.uchicago.edu  
CONTRACT NUMBER: R01 MH59535 (NIMH)  
R01 MH65560-01 (NIMH)  
U01 H46274  
U01 H46282  
U01 MH46280 (NIMH)  
SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (2003 May) 72 (5)  
1131-40.  
Journal code: 0370475. ISSN: 0002-9297.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
OTHER SOURCE: GENBANK-AY170469; GENBANK-AY170470; GENBANK-AY170471;  
GENBANK-AY223901  
ENTRY MONTH: 200307  
ENTRY DATE: Entered STN: 20030422  
Last Updated on STN: 20030702  
Entered Medline: 20030701

AB Linkage evidence suggests that chromosome 13 (**13q32-33**) contains  
susceptibility genes for both bipolar disorder and schizophrenia.  
Recently, genes called "G72" and "G30" were identified, and polymorphisms  
of these overlapping genes were reported to be associated with  
schizophrenia. We studied two series of pedigrees with bipolar disorder:  
the Clinical Neurogenetics (CNG) pedigrees (in which linkage to illness

had been previously reported at **13q32-33**), with 83 samples from 22 multiplex families, and the National Institute of Mental Health (NIMH) Genetics Initiative pedigrees, with 474 samples from 152 families. Sixteen single-nucleotide polymorphisms (**SNPs**) were genotyped at and around the G72/G30 locus, which covered a 157-kb region encompassing the entire complementary DNA sequences of G72 and G30. We performed transmission/disequilibrium testing (TDT) and haplotype analysis, since a linkage-disequilibrium block was present at this gene locus. In the CNG and NIMH data sets, the results of global TDT of the entire haplotype set were significant and consistent ( $P=.0004$  and  $P=.008$ , respectively). In the CNG series, the associated genotypes divided the families into those with linkage and those without linkage (partitioned by the linkage evidence). Analysis of the decay of haplotype sharing gave a location estimate that included G72/G30 in its 95% confidence interval. Although statistically significant association was not detected for individual **SNPs** in the NIMH data set, the same haplotype was consistently overtransmitted in both series. These data suggest that a susceptibility variant for bipolar illness exists in the vicinity of the G72/G30 genes. Taken together with the earlier report, this is the first demonstration of a novel gene(s), discovered through a positional approach, independently associated with both bipolar illness and schizophrenia.

L4 ANSWER 3 OF 41 MEDLINE DUPLICATE 3  
 ACCESSION NUMBER: 2003209405 IN-PROCESS  
 DOCUMENT NUMBER: 22616115 PubMed ID: 12730718  
 TITLE: High-density **SNP** map of human ITR, a gene associated with vascular remodeling.  
 AUTHOR: Iida Aritoshi; Tanaka Toshihiro; Nakamura Yusuke  
 CORPORATE SOURCE: Laboratory for Genotyping, RIKEN SNP Research Center, c/o RIKEN Yokohama Institute, Kanagawa 230-0045, Japan.  
 SOURCE: JOURNAL OF HUMAN GENETICS, (2003) 48 (4) 170-2.  
 PUB. COUNTRY: Japan  
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
 LANGUAGE: English  
 FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals  
 ENTRY DATE: Entered STN: 20030506  
 Last Updated on STN: 20030506

AB We constructed a high-density map of single-nucleotide polymorphisms (**SNPs**) present within a 31-kb region of human chromosome **13q31** that contains the human counterpart of the rabbit ITR gene, which encodes a rhodopsin-like G protein-coupled receptor associated with vascular remodeling. The elements of human ITR cDNA were distributed in 27,452 bp of genomic DNA; the nine exons ranged in size from 50 bp to 2271 bp, with an average size of 392 bp. We isolated a total of 22 **SNPs** from the ITR locus by systematically screening genomic DNA from 48 healthy Japanese individuals; three **SNPs** were present in the 5' flanking region, two in coding elements, 12 in introns, and five in the 3' untranslated region. By comparing our data with **SNPs** deposited in the dbSNP database in the National Center for Biotechnology Information, 19 of the 22 **SNPs** (86%) were considered to be novel. The map presented here should help in evaluating the role of human ITR in cardiovascular diseases, in other diseases mapped to this segment on chromosome **13q31**, and in a variety of pharmacogenetic effects.

L4 ANSWER 4 OF 41 SCISEARCH COPYRIGHT 2003 THOMSON ISI  
 ACCESSION NUMBER: 2003:68630 SCISEARCH  
 THE GENUINE ARTICLE: 631VE  
 TITLE: Association of neuregulin 1 with schizophrenia confirmed in a Scottish population  
 AUTHOR: Stefansson H (Reprint); Sarginson J; Kong A; Yates P; Steinthorsdottir V; Gudfinnsson E; Gunnarsdottir S; Walker N; Petursson H; Crombie C; Ingason A; Gulcher J R;

Stefansson K; St Clair D  
CORPORATE SOURCE: DeCODE Genet, Sturlugata 8, IS-101 Reykjavik, Iceland  
(Reprint); DeCODE Genet, IS-101 Reykjavik, Iceland; Natl  
Univ Hosp Reykjavik, Dept Psychiat, Reykjavik, Iceland;  
Univ Aberdeen, Sch Med, Aberdeen AB9 2ZD, Scotland;  
Aberdeen Royal Infirm, Aberdeen, Scotland; Ravenscraig  
Hosp, Greenock, Scotland  
COUNTRY OF AUTHOR: Iceland; Scotland  
SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (JAN 2003) Vol. 72,  
No. 1, pp. 83-87.  
Publisher: UNIV CHICAGO PRESS, 1427 E 60TH ST, CHICAGO, IL  
60637-2954 USA.  
ISSN: 0002-9297.  
DOCUMENT TYPE: Article; Journal  
LANGUAGE: English  
REFERENCE COUNT: 32

\*ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS\*

AB Recently, we identified neuregulin 1 (NRG1) as a susceptibility gene for schizophrenia in the Icelandic population, by a combined linkage and association approach. Here, we report the first study evaluating the relevance of NRG1 to schizophrenia in a population outside Iceland. Markers representing a core at-risk haplotype found in Icelanders at the 5' end of the NRG1 gene were genotyped in 609 unrelated Scottish patients and 618 unrelated Scottish control individuals. This haplotype consisted of five **SNP** markers and two microsatellites, which all appear to be in strong linkage disequilibrium. For the Scottish patients and control subjects, haplotype frequencies were estimated by maximum likelihood, using the expectation-maximization algorithm. The frequency of the seven-marker haplotype among the Scottish patients was significantly greater than that among the control subjects (10.2% vs. 5.9%,  $P = .00031$ ). The estimated risk ratio was 1.8, which is in keeping with our report of unrelated Icelandic patients (2.1). Three of the seven markers in the haplotype gave single-point  $P$  values ranging from .000064 to .0021 for the **allele** contributing to the at-risk haplotype. This direct replication of haplotype association in a second population further implicates NRG1 as a factor that contributes to the etiology of schizophrenia.

L4 ANSWER 5 OF 41 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.DUPLICATE  
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ACCESSION NUMBER: 2003:32120 BIOSIS  
DOCUMENT NUMBER: PREV200300032120  
TITLE: Schizophrenia associated genes, proteins and  
**biallelic** markers.  
AUTHOR(S): Cohen, Daniel (1); Blumenfeld, Marta; Chumakov, Ilya;  
Bougueleret, Lydie; Bihain, Bernard; Essioux, Laurent  
CORPORATE SOURCE: (1) Neuilly-Sue-Seine, France France  
ASSIGNEE: Genset, France  
PATENT INFORMATION: US 6476208 November 05, 2002  
SOURCE: Official Gazette of the United States Patent and Trademark  
Office Patents, (Nov. 5 2002) Vol. 1264, No. 1, pp. No  
Pagination. <http://www.uspto.gov/web/menu/patdata.html>.  
e-file.  
ISSN: 0098-1133.  
DOCUMENT TYPE: Patent  
LANGUAGE: English

AB The invention concerns the human sbg1, g34665, sbg2, g35017 and g35018 genes, polynucleotides, polypeptides **biallelic** markers, and human chromosome **13q31-q33** **biallelic** markers. The invention also concerns the association established between schizophrenia and bipolar disorder and the **biallelic** markers and the sbg1, g34665, sbg2, g35017 and g35018 genes and nucleotide sequences. The invention provides means to identify compounds useful in the treatment of schizophrenia, bipolar disorder and related diseases, means to determine

the predisposition of individuals to said disease as well as means for the disease diagnosis and prognosis.

L4 ANSWER 13 OF 41 CAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:417174 CAPLUS

DOCUMENT NUMBER: 135:44766

TITLE: The human gene g35030 associated with schizophrenia, the gene product and **biallelic** markers for determination of risk

INVENTOR(S): Cohen, Daniel; Blumenfeld, Marta; Chumakov, Ilya; Bougueleret, Lydie; Essioux, Laurent

PATENT ASSIGNEE(S): Genset, Fr.

SOURCE: PCT Int. Appl., 424 pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 5

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001040493	A2	20010607	WO 2000-IB1507	20001004
WO 2001040493	A3	20020718		
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
EP 1242606	A2	20020925	EP 2000-966375	20001004
R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL			

PRIORITY APPLN. INFO.: US 1999-168088P P 19991130

WO 2000-IB1507 W 20001004

AB The invention concerns the human g35030 gene, polynucleotides, polypeptides **biallelic** markers, and human chromosome **13q31-q33 biallelic** markers. The invention also concerns the assocn. established between schizophrenia and bipolar disorder and the **biallelic** markers and the g35030 gene and nucleotide sequences. The invention provides means to identify compds. useful in the treatment of schizophrenia, bipolar disorder and related diseases, means to det. the predisposition of individuals to said disease as well as means for the disease diagnosis and prognosis.

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